

SEQUENCE LISTING

<110>Suntory Limited et al.

<120>Proess for production of yellow flowers by control of flavonoid synthesis system

<130>P952

<160>70

<210>1

<211>1422

<212>DNA

<213>

<220>

<221>

<222>

<223>Nucleic acid in pSPB1725

<400>1

atg gga gaa gaa tac aag aaa aca cac aca ata gtc ttt cac act tca 48

Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser

1 5 10 15

gaa gaa cac ctc aac tct tca ata gcc ctt gca aag ttc ata acc aaa 96

Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys

20 25 30

cac cac tct tca atc tcc atc act atc atc agc act gcc ccc gcc gaa 144

His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu

35 40 45

tct tct gaa gtg gcc aaa att att aat aat ccg tca ata act tac cgc 192

Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg

50 55 60

ggc ctc acc gcg gta gcg ctc cct gaa aat ctc acc agt aac att aat 240

Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn

65 70 75 80

aaa aac ccc gtc gaa ctt ttc ttc gaa atc cct cgt cta caa aac gcc 288

Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala

85 90 95

aac ctt cga gag gct tta cta gat att tcg cga aaa tcc gat atc aaa 336

Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys

100 105 110

gca tta atc atc gat ttc ttc tgc aat gcg gca ttt gaa gta tcc acc	384
Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr	
115 120 125	
agc atg aac ata ccc act tac ttc gac gtc agt ggc ggc gct ttt ctc	432
Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu	
130 135 140	
ctc tgc acg ttt ctc cac cac ccg aca cta cac caa act gtt cgt gga	480
Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly	
145 150 155 160	
gac att gcg gat ttg aac gat tct gtt gag atg ccc ggg ttc cca ttg	528
Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu	
165 170 175	
att cac tcc tct gat tta cca atg agt ttg ttt tat cgt aag act aat	576
Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn	
180 185 190	
gtt tac aaa cac ttt cta gac act tcc tta aac atg cgc aaa tcg agt	624
Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser	
195 200 205	
ggg ata ctc gtg aac acg ttt gtt gcg ctc gag ttt cga gct aag gaa	672
Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu	
210 215 220	
gct ttg tcc aac ggt ttg tac ggt cca act ccg cct ctt tat tta ctt	720
Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu	
225 230 235 240	
tca cat aca att gcc gaa ccc cac gac act aaa gtg ttg gta aac caa	768
Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln	
245 250 255	
cac gaa tgc cta tca tgg ctt gat ttg cag cct agt aaa agc gtg att	816
His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile	
260 265 270	
ttc ctt tgt ttc gga aga aga gga gcg ttc tca gca caa cag ttg aaa	864
Phe Leu Cys Phe Gly Arg Arg Gly Ala Phe Ser Ala Gln Gln Leu Lys	
275 280 285	
gaa att gcg ata ggg ttg gag aag agt gga tgt cga ttt ctt tgg ttg	912
Glu Ile Ala Ile Gly Leu Glu Lys Ser Gly Cys Arg Phe Leu Trp Leu	
290 295 300	

gcc cgc att tca ccg gag atg gac tta aat gcg ctt ctg ccg gag ggt	960
Ala Arg Ile Ser Pro Glu Met Asp Leu Asn Ala Leu Leu Pro Glu Gly	
305 310 315 320	
ttt cta tcg aga act aaa gga gta ggg ttt gtg aca aac aca tgg gtg	1008
Phe Leu Ser Arg Thr Lys Gly Val Gly Phe Val Thr Asn Thr Trp Val	
325 330 335	
ccg caa aaa gag gtg ttg agt cat gat gca gtg ggg ggg ttt gtg act	1056
Pro Gln Lys Glu Val Leu Ser His Asp Ala Val Gly Gly Phe Val Thr	
340 345 350	
cat tgc ggg tgg agt tcg gtt ctt gaa gcg ctg tcg ttc ggt gtc ccg	1104
His Cys Gly Trp Ser Ser Val Leu Glu Ala Leu Ser Phe Gly Val Pro	
355 360 365	
atg att ggt tgg ccg ttg tac gca gag cag agg atc aat agg gtg ttc	1152
Met Ile Gly Trp Pro Leu Tyr Ala Glu Gln Arg Ile Asn Arg Val Phe	
370 375 380	
atg gtg gag gaa ata aag gtg gcg ctg cca ttg gat gag gaa gat gga	1200
Met Val Glu Glu Ile Lys Val Ala Leu Pro Leu Asp Glu Glu Asp Gly	
385 390 395 400	
ttt gtg acg gcg atg gag ttg gag aag cgc gtc agg gag ttg atg gag	1248
Phe Val Thr Ala Met Glu Leu Glu Lys Arg Val Arg Glu Leu Met Glu	
405 410 415	
tcg gta aag ggg aaa gaa gtg aag cgc cgt gtg gcg gaa ttg aaa atc	1296
Ser Val Lys Gly Lys Glu Val Lys Arg Arg Val Ala Glu Leu Lys Ile	
420 425 430	
tct aca aag gca gcc gtg agt aaa ggt gga tcg tcc ttg gct tct ttg	1344
Ser Thr Lys Ala Ala Val Ser Lys Gly Gly Ser Ser Leu Ala Ser Leu	
435 440 445	
gag aag ttc atc aac tcg gtc act cgt taaag tttcttactc aatatatggt	1396
Glu Lys Phe Ile Asn Ser Val Thr Arg	
450 455	
acatcggttt aactaccaaa ttttat	1422

<210>2

<211>457

<212>PRT

<213>

<223>Amino acid sequence of 4,2',4',6'-tetrahydroxychalcane 4'-O-glycosyltransferase encoded in pSPB1725

<400>2

```

Met Gly Glu Glu Tyr Lys Lys Thr His Thr Ile Val Phe His Thr Ser
  1             5             10             15
Glu Glu His Leu Asn Ser Ser Ile Ala Leu Ala Lys Phe Ile Thr Lys
          20             25             30
His His Ser Ser Ile Ser Ile Thr Ile Ile Ser Thr Ala Pro Ala Glu
          35             40             45
Ser Ser Glu Val Ala Lys Ile Ile Asn Asn Pro Ser Ile Thr Tyr Arg
          50             55             60
Gly Leu Thr Ala Val Ala Leu Pro Glu Asn Leu Thr Ser Asn Ile Asn
          65             70             75             80
Lys Asn Pro Val Glu Leu Phe Phe Glu Ile Pro Arg Leu Gln Asn Ala
          85             90             95
Asn Leu Arg Glu Ala Leu Leu Asp Ile Ser Arg Lys Ser Asp Ile Lys
          100            105            110
Ala Leu Ile Ile Asp Phe Phe Cys Asn Ala Ala Phe Glu Val Ser Thr
          115            120            125
Ser Met Asn Ile Pro Thr Tyr Phe Asp Val Ser Gly Gly Ala Phe Leu
          130            135            140
Leu Cys Thr Phe Leu His His Pro Thr Leu His Gln Thr Val Arg Gly
          145            150            155            160
Asp Ile Ala Asp Leu Asn Asp Ser Val Glu Met Pro Gly Phe Pro Leu
          165            170            175
Ile His Ser Ser Asp Leu Pro Met Ser Leu Phe Tyr Arg Lys Thr Asn
          180            185            190
Val Tyr Lys His Phe Leu Asp Thr Ser Leu Asn Met Arg Lys Ser Ser
          195            200            205
Gly Ile Leu Val Asn Thr Phe Val Ala Leu Glu Phe Arg Ala Lys Glu
          210            215            220
Ala Leu Ser Asn Gly Leu Tyr Gly Pro Thr Pro Pro Leu Tyr Leu Leu
          225            230            235            240
Ser His Thr Ile Ala Glu Pro His Asp Thr Lys Val Leu Val Asn Gln
          245            250            255
His Glu Cys Leu Ser Trp Leu Asp Leu Gln Pro Ser Lys Ser Val Ile

```

	260		265		270										
Phe	Leu	Cys	Phe	Gly	Arg	Arg	Gly	Ala	Phe	Ser	Ala	Gln	Gln	Leu	Lys
	275						280					285			
Glu	Ile	Ala	Ile	Gly	Leu	Glu	Lys	Ser	Gly	Cys	Arg	Phe	Leu	Trp	Leu
	290						295					300			
Ala	Arg	Ile	Ser	Pro	Glu	Met	Asp	Leu	Asn	Ala	Leu	Leu	Pro	Glu	Gly
305					310					315				320	
Phe	Leu	Ser	Arg	Thr	Lys	Gly	Val	Gly	Phe	Val	Thr	Asn	Thr	Trp	Val
			325						330					335	
Pro	Gln	Lys	Glu	Val	Leu	Ser	His	Asp	Ala	Val	Gly	Gly	Phe	Val	Thr
			340					345					350		
His	Cys	Gly	Trp	Ser	Ser	Val	Leu	Glu	Ala	Leu	Ser	Phe	Gly	Val	Pro
	355						360					365			
Met	Ile	Gly	Trp	Pro	Leu	Tyr	Ala	Glu	Gln	Arg	Ile	Asn	Arg	Val	Phe
	370					375						380			
Met	Val	Glu	Glu	Ile	Lys	Val	Ala	Leu	Pro	Leu	Asp	Glu	Glu	Asp	Gly
385					390					395				400	
Phe	Val	Thr	Ala	Met	Glu	Leu	Glu	Lys	Arg	Val	Arg	Glu	Leu	Met	Glu
			405						410					415	
Ser	Val	Lys	Gly	Lys	Glu	Val	Lys	Arg	Arg	Val	Ala	Glu	Leu	Lys	Ile
			420					425					430		
Ser	Thr	Lys	Ala	Ala	Val	Ser	Lys	Gly	Gly	Ser	Ser	Leu	Ala	Ser	Leu
	435						440					445			
Glu	Lys	Phe	Ile	Asn	Ser	Val	Thr	Arg							
	450					455									

<210>3

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Morning glories 3GGT

<400>3

gaaatggtcg gattggctgg g

<210>4
 <211>21
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer for cloning DNA encoding Morning glories 3GGT
 <400>4
 acctccaccc caactttcag g 21

<210>5
 <211>24
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer for cloning DNA encoding Petunia 3GT
 <400>5
 gatgcataat ttggctagaa aagc 24

<210>6
 <211>21
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer for cloning DNA encoding Petunia 3GT
 <400>6
 ccaatttgcc aaacactttc c 21

<210>7
 <211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Verbena 5GT

<400>7

tgcctcgaat ggttgagcac g

21

<210>8

<211>18

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Verbena 5GT

<400>8

ctctcactct cacacccg

18

<210>9

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Baicalein GT

<400>9

cacgaatgct tagcatggct c

21

<210>10

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Baicalein GT

<400>10

cttattgccc actgaaaccc c

21

<210>11

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Gentiana 3'GT

<400>11

tgtctgaatt ggcttgattc c

21

<210>12

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer for cloning DNA encoding Gentiana 3'GT

<400>12

aaccacaga aaccctgtt c

21

<210>13

<211>1446

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB264

<400>13

atgggaaaac ttcacattgc cttatttcca gttatggctc atggtcacat gatcccaatg	60
ttggacatgg ccaagctctt tacctcaaga ggcatacaaa caacaatcat ttcgactctc	120
gccttcgctg atccgataaa caaagctcgt gattcgggcc tcgatattgg actaagcatc	180
ctcaaattcc caccagaagg atcaggaata ccagatcaca tggtagcct tgatctagtt	240
actgaagatt ggctcccaaa gtttgttgag tcattagtct tattacaaga gccagttgag	300
aagcttatcg aagaactaaa gctcgactgt ctcgtttccg acatgttctt gccttggaca	360
gtcgattgtg cggctaagtt cggatttccg aggttggttt tccacggaac gagcaacttt	420
gcgttgtgtg cttcgagca aatgaagctt cacaagcctt ataagaatgt aacttctgat	480
actgagacat ttgttatacc ggatttcccg catgagctga agtttgtgag gactcaagtg	540
gctccgtttc agcttgcgga aacggagaat ggattctcaa agttgatgaa acagatgacg	600
gagtcgttg gtagaagcta cgggtgtgtg gttaacagtt tttatgagct cgagtcgact	660
tatgtggatt attacagaga ggttttgggt agaaagtctt ggaatatagg gcctctgttg	720
ttatccaaca atggcaatga ggaaaaagta caaaggggaa aggaatctgc gattggcgaa	780
cacgaatgct tggcttgggt gaattccaag aagcagaatt cggttgttta cgtttgtttt	840
ggaagtatgg cgacttttac tccagcgagc ttgcgcgaaa ctgcgattgg actcgaggaa	900
tcaggccaag agttcatttg ggtagttaaa aaggccaaaa acgaagaaga aggaaaagga	960
aaagaagaat ggctgccaga aaattttgag gaaagagtga aagatagagg cttgatcata	1020
agaggatggg cgccgcaatt gttgatactc gatcatcctg cggtaggagc tttcgtgacg	1080
catttgtgat ggaattcgac gttggaagga atatgcgccg gtgtgcctat ggtgacttgg	1140
ccagttttcg cagagcagtt tttcaatgag aagtttgtga cagaggtttt ggggaccggt	1200
gtttcggttg ggaataagaa gtggctaagg gcagcaagtg aagggtgtgtc gagggaggca	1260
gtgacgaacg cggcgcagcg tgttatggtg ggagaaaatg cgtcggagat gagaaagcga	1320
gcgaagtatt ataaggaaat ggcgaggcgg gcggttgagg aaggcggttc gtcttataat	1380
ggtttgaatg agatgataga ggatttgagt gtgtaccgtg ctccagaaaa acaagactta	1440
aactag	1446

<210>14

<211>1488

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB662

<400>14

atggcctttc aaattcaacc agagcttcta aacttcgttt tcataccatt catggccccct	60
ggccactcaa tccctatgat agacttagcc aaattattcg cggaacgcgg cgtcaacgta	120
acgatcatcg taacacctct taacgccgca cgattcaatt ccgttattaa tcgagccggt	180
gaatcaggac agtccattcg tcttctccaa gtaaaattcc ctggtgaaga agccggggtg	240
ccacctggat gcgaaagcgc cgagacttta ccatcttatg aattgattcc aaatTTTTTT	300
accgccgtaa aaatgttaca acaaccaatc gaggaagaat tgagaaattt gatcccttta	360
ccaagctgcg tcatttgtga taaacacata ccctggactg ctcaaacgtg caagaatctc	420
cgaattccga ggataatttt cgatggaatg agctgttttg ctcccttagt aacacacgtt	480
ctctacgtgt ctaaggttca tgaaaccgtt cctccaaacg agccgttcgt tgttcctgat	540
ttccccgatg agatagagtt aacgaggttt caattgccag ggttgttgaa tccaagtcca	600
aggataaatt tttacgattt tcgcaacaaa gtgaagaaaa ctgaggagga ggcttatggg	660
gtggtggtga acagttttga ggagctggaa aaagattatt tcgagatggt tcggaaattg	720
aaagggggta aagtttggtg tgttgggcct ttgtcgcttt atggtaacga cgatttgac	780
agggctggaa gagggaataa ggcgtcgatt gatacggatc ggtgtatgaa atggcttgat	840
gataatgaac cagaatctgt aatttatgcc tgtttgggaa gcctgagtcg tttgtcgcgt	900
tcacagttcg tcgaacttgc tttgggattg gaagcatcaa aacactcggt tgttctagtt	960
gttaaaaccg aaggagagaa gtcgttggaa atagagaaat ggattttgga caatggattc	1020
gaggaaagaa cgaaagatag agggttcttg attcgtggtt ggtcgccaca agtgttgatc	1080
ttgtcgcatt ttgcagtggg aggattcttg acgcatttgt gttggaattc gacgcttgag	1140
ggcatttgtg ctggtttgcc aatggtgatg tggccgatgt tcggcgaaca gtttttgaat	1200
gagaagttag tgggtgcagat tttggggacg ggtgtgggag ttggagcgaa aagtacggta	1260
catttggggg atgaagagat ggatgagatg agagtacga ggaaggggat taccaaggcg	1320
gtcgtggcag ttatggatag aggaactgaa ggggtgtgaga ggcgagagaa ggcgaaggag	1380
cttggtgaaa tggctaagag ggcagtccaa gttgggggat cttcatgtaa gaatgtcgac	1440
cagctaattc aagaagtgc accattgagt gtagcgaggg atgtgtaa	1488

<210>15

<211>1446

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1621

<400>15

atgggttctc tccctgaaaa tgagctcaac aaaccacatg ctgtgtgcat accctatcca	60
---	----

gcactagggc atttcagtcc catgctagat ttigtctaagc tcctccacca aaaaggcttt	120
cacataacct tcgtcaacac cgagtacatc cgtctccgcc tcctcaagtc ctgtggccct	180
gccgccctgg acgggctacc ggactttcgc ttcatgacta tccccgatgg cctccctttg	240
tcggacgacg tttcgcgtga tgtcgcttcc atttctgtct ctactaacia aacttgctta	300
gaaccctttt gtgaggtgct atcggacctc atggataatg gttccaaccc gccggtgagc	360
tgcatttgtgt ccgacggggg aatgagtttc acccttgagg cggcggagag gtttggactg	420
ccagaggtgc tgttctggac gcccgctgct tgtggcatct tagctttcac gcagtataag	480
catcttgttg agagaggata tgtacctctc aaagatacga gccaggtaac aaatggctac	540
ctggaaacia tattagattg ggttccaggg atgaaggata ttcgattgag ggaattccca	600
actttcataa gaacgacgga cccaaacgac gttatgctgg attttctaata aaaacaagtt	660
gacgccaccc cgaaagccaa tgctgtgatc atcaacacgt tcgacacatt ggaaagtgac	720
gctctcaacg ccctctctgt catgtttccg cgcatataca cactcgggcc tctccatatg	780
atgttgaata atccccaggt cgacgaaccc tctaatacaa tcaaatttaa tctttggaaa	840
gaagactcac attgcctaga ttggctcgat gtgaacgagc ccggaacagt tgtatacgtg	900
aattttggca gctcaacaat tctgactgtt gaacaactaa ctgaattagc atggggcctt	960
gctaacagca agaaaccgtt cctttggatc atcaggcctg atttagtaac tggatgcatcc	1020
tccatgcttc cgcttgagtt cctggctcgag actaaagaca gaagcatgtt agtgagttgg	1080
tgcaaccaag aacaagtgtt gaagcacccc gcgactggag tgttcttgac gcattgtgga	1140
tggaaattcga cgattgaaag catttgcagc ggcgtgccaa tgatttggtg gccttactac	1200
gctgagcagc aaaccaactg taggtacagt tgtgtggaat gggaaatagg aatggagatc	1260
attgacaacg atgtgaagag agatgaggtg gaattgctgg tgattaagtt gatggatggt	1320
atcaagggaa agaaaatgaa aaagaaagct atggagtggg agaggaaagc agaagaggcg	1380
gtagcttttg ggggctcttc ctacatgaat ttggataaac ttattagcga cgtgcttttt	1440
ccataa	1446

<210>16

<211>1458

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1620

<400>16

atggcaggtc caaattgcaa gcctcacgcc atcatgatcg cacttcctta ccaaggccac	60
ataactcctt ttgtcaatct tgcactaaaa cttgcttcca atggctttac aatcactttt	120

gttcaccttg aatttatcca ccaaatgttg tctaaagccc ataacgccac taaaactgaa	180
gcagatttat ttctggaagc acgagaatcc ggtctcgaca tacgttacac aacgattgac	240
gatggtttcc ctttggaatt cgacagggct ctccactccg aggagtattg gcactccatg	300
ttgcgagatt tcccgttaca cgtcgatgag tttgttcgaa aagtcgtgga gtcagagcca	360
tttttagagc acttttttgt tacggatact atgtatacat ggccctgcaac cattgcaaag	420
aaacataatc ttgtgaatat ttcgtttttg actgaaccag ccctgggtgtt ttctttgtct	480
taccatataa accttctgaa gcaaaatggt cattttccat gttaaagaaaa tattgatgag	540
gaaataaatt acgtaccagg agttgattca ataagtacaa gggatttaat gtcttatttt	600
aaagaaccag gatcagaaac attagagaaa aatgtttgtc tcaaggcatt tgaaggagtg	660
aagaaagctg atttcatctt gcataacaca ttgcaagaac tagaatctga gacactctca	720
gtctttacca aaatgcagcc aaattacgcc gttggacctt ttaatttctc caaacatact	780
cctaaaactg tcaccaagag tctacggtct gaattcgact gcaccaactg gctcgactct	840
aagcctccca actctatttt atacgtctcg tttggtagtt ttattcagac aagcaaagag	900
gtaattgaag aaatcgctta cggctttctc cttagtgaag ttaactttat atgggtggtt	960
agaacagata gtgtgagttt agaggataac gaggttttgc cggttggatt tagggatgag	1020
gttaaagata gggggttgat agttccgtgg tgtgatcaaa ttacggtttt gtctaatacgc	1080
gcggttggag gattcttgac gcattgtgga tggaactcgg tattagagag tatgtggtgt	1140
ggcgttccta tgatttgta tccgttaaca tatgatcaac ctactaatag gaaactattg	1200
gttgatgatt ggaagattgg cattaatctt tgcgacggag cgttgattaa tagaaaagaa	1260
attgcagaga agattaaggc cttgatgagt gaaagtactt cagaggggtt gagggaagaa	1320
tctgagaaag ttaagggctt gttgaagaat gcactggaag ttggtggttc atcagagaag	1380
aatttcaata aatttattga ggatttgaag gcaaaaattc aaataatgaa agagcaaag	1440
cctgctaata ccagttga	1458

<210>17

<211>1443

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1622

<400>17

atgggttcca cagccgaaaa taaacagaaa acccacattg tgtgcatacc ctaccagcc	60
caggggcaca tcagcccat gctaaagtta gccaaactgc tacacaaaa cggcttttac	120
atcacttttg tcaacacgga gtacaaccac cgccgcctca tcaagtcccg cgccccacc	180

gccctcgacg gattgcccga tttccggttc gttacgatcc ccgacgggct tcctttctct	240
gaagccgacg ccacacagga tatcccttct ctttgtgttt caaccaccaa cacttgcttg	300
gagccctttt gcgagctgct gtcgaacctc aataactccg gcccggacgt gccccgggtg	360
agctgcatcg tatccgatgg tgtcatgagc ttcacgttga aggcggcgga gagatttggg	420
ctgccggagg tgctgttctg gacgacgagt gcgtgtgggt tcttggcgta tacgcagtat	480
aagcatctcg tggagaaagg ctatgtaccc ctcaaagata tgagccaagt aacggatgga	540
tatttgaana caagcatgga ctggattcca ggaacgaagg acatccaact aagggaacttc	600
ccctctttca tcaggacaac agatccagaa gacatcatgc ttaatttttt aatacaagaa	660
actgatgttg ttccgagagc caaagctgta ataataca ccttcgacat gttagaacac	720
gacgtcctgg aagcgctctc caccatgttt tcacgcgttt acagcatcgg ccctcttcag	780
ctgatgatga attatgttca caacgagtc cttaaatcca tcagttccag tctatggaaa	840
gaagaaacac attgcgtcga ttggctcgat tcaaaggagc ccgaatccgt tgtgtacgta	900
aattttggca gcataactgt cgtgactgca gaacaactga ctgagtttgc gtgggggctc	960
gctaatagta agaagacttt cctatgggtt attaggcctg atatagttgc tggagactcg	1020
gctatgctgc ccctgaatt cgtgacgggg acaaaagata gaagcatgtt aatcagctgg	1080
tgtaaccaag aacaggtgtt gaatcaccca tcaattggag ggtttttgac gcacagtgg	1140
tggaattcga cgattgaaag tatagtcgag ggagttcctg tgatttgctg gcctttcttt	1200
gctgagcagc aaacaaattg taggttcagt tgcgtggaat gggaaatagg aatggagatt	1260
gataataatg tgaagagaga tgaggttgaa gtttttggtga gggaattgat ggatggagag	1320
agggggaaga aaatgaagga gaaagctatg gagtggaaag ggaaagcatt agaggcaact	1380
gcacttgggg gctcttccta ctgaacttg gaaaaactaa ttaaggaggt gcttttgc	1440
taa	1443

<210>18

<211>1407

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1610

<400>18

atggcatctt ctccccataa ccagccaacc acgccccgcc acgtggtggc cctaccctac	60
cccgccgcg gccacataaa ccccatgctc aacatctgca aagccgtagc ggagaagagc	120
agccacatca acataacaat catcctaacc gaggaatggc tcggcttaat cggctcagcc	180
gacaagccgc cgaacataag ctacgccgcg ataccgaaca ttctgccgtc ggagcacgtt	240

cgcgggcgagg atccacatgg tttttgggcg gctgtttggc agaagatgga ggagccggtt	300
gatcggctgc tggacgagct tcggcttaat aataacaagc cggagtttgt gatagccgat	360
gctttcttgc attgggcggc tgacgtggcg ggcaggagga atattccctt ggcatctgtt	420
tggccaatgt cggcgtccac gtacacggtg ctttaccact ttgaccttct cgttgaccac	480
ggacactttc cgatcgacat accagtgaat ggagatgcta ttgtggatta catcccggga	540
ctccctccag ttcgctcgc agattttcca aaagacataa gaaaacaaga agacgcatcc	600
ttcgtcctta aactcattcc caactcacca aaattcatca tcttcacttc aatttacgac	660
ctcgaatcca agatcatcga cgctctaaag caaaaatctt ccttctcaat ctacaacatt	720
ggctctcatg ctctctattc caaactcaaa cacatcctca actcggataa aatcacgaaa	780
cctgatcaag ataaccccga ctacttaaaa tggttagatc tccaacctcc caactccgtc	840
ttgtacattt cactcggcag ttctctatcc atttcgcgag cccaaatgga tgaactcgca	900
accggaatac gaaactctgg tgtccgcttt ttgtgggtgg cacgtggcga aacaaaccgg	960
ttgaaagaga ttgtttgtga tcatgaaaag gggctgatca tagaatggtg cgatcaaag	1020
caggttcttt ctcatcttc ggttgggtgga ttcttgtcgc attgtggttg gaattcgact	1080
aaagaggcgt tgatggccgg ggtgccgttt ttgactattc caattatgtt tgatcaagtg	1140
tctaacgcga aggcggctcgt ggaagattgg aggggtgggt ggagggtggt gaatgagttt	1200
aatgaagaag agttgggtggg aggagatgag attgcgaata ttgtgaggag gtttatggat	1260
atggaaaatg gtgagaggaa agagttgacg aaaaatgtga aagagggtgca gaagatttgt	1320
gcgagagagt tcgaagatgg agatggacag tcgtttgagt ttaatgttga aagtttggtt	1380
caattgattc tgcaattggg tccgtaa	1407

<210>19

<211>1428

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1609

<400>19

atgaacaaca caacccaaca acaaacagta gcattagcac tagcacctca ctgtttaatc	60
gtcccatctc cattccaagg ccacattaac cccttactcc aattcgccaa acgcctcata	120
actcaccaca acaaaaacct ccaaatacaca ttcgcactca ccaaattcat cctcaccaac	180
ctctcctccg gtgccggaga atcatccttc tctctccggt caatctccga cggcttcgac	240
gccggcggcc gcgctcaggc caactccggc gccgaatacc tctccaaatt ccgcgagatc	300
ggatctcaaa ccctaaccga acttatccaa gacctatccg aatcggtcgc acccgttgac	360

tgcgtggtct acgacccgtt cgtaccttgg gccttagatg ttgccaaggg taaattcgga	420
atttcaacgg cggcgttttt tacgcagtcg tgtgcggtgg ataatatata cagtcggggtt	480
tataacggcg atttggagct gccgttgccg gagaatgagg tggtaggggt tccggggttg	540
ccggagatgg agccgtttga gatgccgagc tttgtgtatt taaacgggtc gtacccgtcg	600
agttttgaga tggttgtggg tcagtttagg aatgttgatg aggcggattg ggtttttgtc	660
aacacttttt atgagttgga gaaagaggtc attgactgga tgtcaaaatc ttggcgagtg	720
aaagcaattg gacctaccat accatcaatg ttcatggaca agagattgca agaggacaaa	780
tcatacggtc ttagcatgtt caagcataca acaaatgact gcataaatig gctcaacgga	840
aaacaatcaa aatccgtcat ttatgtcgca ttggaagtc ttgcagaatt atcccacgac	900
caaactcaag aactggcaca cgccttaaca acctacgaca aacacttctt atgggttgta	960
cgatcatcgg aagaagctaa gcttcccca aattttgcta acgaaacatc taagaaaggg	1020
ttgatagtgt cgtggtgccc tcaattagag gtcttgtcgc acgaggccat cggttgtttc	1080
gtgactcatt gtggttgga ttcaacgctc gagggattga gtttgggggt gcctatgggtg	1140
gcgatgccac agtggacgga tcagagtacg aacgctaagt ttatcgtgga tgtttgggggt	1200
gtgggtgttc gggctaaggt ggacgagggg ggattagcga ggcaagatga gatagttcgt	1260
tgcttaggga gcgtcatgga agggggagaac ggagaaaaga taagaaagaa tgcgaatgaa	1320
tggaaggaac gggcgtgcaa tgcagttgat gaagggggga gttcagacaa aaatattgaa	1380
gaatttgtaa ctacgttgat aagtcccat gacttgcgtc aagagtaa	1428

<210>20

<211>1425

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1617

<400>20

atgtctagtg agagccaaat aaacttagtg ttcatccctc tccctgtaaa gggacacatt	60
gtctcaacgc tagagacggc aaagctactc gtcgatcgaa acaaacgcct caccatcaca	120
atcctcctca tgaagctgcc agtcgacgcc aaggtagatg attccttcac aaaaaatccc	180
tcctgtcttc aaataacttt tgtacatctc cctcgaaatcg agcacagttc catggaacca	240
ccgggaactc ccgaatcctt tgtacacagg ttcgctcgaga gccaaaaatg tctcgtaaga	300
gatgcggttg ttaaagcaac ggagggctca aaatcaaaca ggctagccgg atttgtaatc	360
gacatgttct gcaccccgat gattgatgtg gccaatgaat ttggcgtccc gacatacgtg	420
gctttcacgt ccggggccgc aactctcggg ctattgttcc atttgcagag tcttagagat	480

gaatttaatc	aggacgtgaa	ggagtacgag	aactcgggaag	ttgagataatc	gatccccggct	540
tatgttaacc	cgttcacctc	caaataccttg	ccgtctcctg	tcttcaacga	ggacgggtgtt	600
tttcttagtc	ttgcaaaggg	gttcagagag	gctaaaggta	tattgatcaa	caccttttta	660
gaatttgaat	cccatgccat	taaatcgctc	tccaacgatg	cgagaatccc	gcctgtttac	720
cccatcgggc	cagtaattca	cgccacggaa	gataatgcaa	acaaaggaaa	gcaggacgaa	780
atcatcgcg	ggcttgacga	gcaacctgat	tcataccgtcg	tgtttctttg	cttcggaagc	840
gctggatgct	ttgaagaaaa	tcaagtgaag	gagattgcag	tggcgctcga	caaaagtgga	900
taccggtttt	tatggtcatt	gagaaagccg	cctcccaaag	aaaaagcgga	gtttccaggg	960
gagtacaaag	attttaatga	agttttacca	gaagggttct	tacaacgtac	gtccgggaga	1020
ggtaaggtaa	taggatgggc	tccgcagatg	gccgtgttgt	ctcacaatgc	ggtgggagga	1080
ttcgtgtcgc	attgcggctg	gaactcgacg	ttggagagtg	tttggtgcgg	agtgccaatg	1140
gccgtgtggc	cattggcggc	cgagcaacat	gcgaacgcgt	tccagttggt	gaaggagtgtg	1200
ggaattgcgg	tggagattaa	gatggattat	aggaagaaca	gtggtgtgat	tgtggaggca	1260
aaaatgattg	agaaaggaat	cagggagtgtg	atggaccg	aaaatgagat	aaggggtaat	1320
gtgaaagtga	tgaaaaagga	gagtaggaNa	gctgtcgtgg	atggtgggac	ttcttttgat	1380
tacttggatc	gttttgttga	aactgtcgtg	aataatgttt	tgtga		1425

<210>21

<211>1446

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1615

<400>21

atgggttccg	tagccggaaa	cagttacaaa	cggcctcatg	ctgtgtgcat	acccttcccc	60
gcgcaggggc	acatcaacc	catgctgaag	ttggccaaac	tcctccacca	aaagggttc	120
cacatcacat	tcgtcaacac	agagtacaac	caccgccgct	tgctcaagtc	cctcggcccc	180
gacgctctcg	atggcttgcc	ggatttccga	ttcgcaacca	tccccgacgg	tcttctctcg	240
tctgacgcgg	acgtcactca	ggatgttcct	tctctttgta	tgtccaccac	taacacttgc	300
ttggagccct	ttaccgagtt	gctgttgaaa	ctcaataact	ccggccccga	cgtgccaccg	360
gtgacctgca	tcgtctcgga	tgggtgcatg	agcttcacat	tgaaggcggc	ggagaggttt	420
gcgctgccgg	aagtgtgtt	ctggacgacg	agtgcgtgtg	gtttcttggc	gtacacgcag	480
tataagcgtc	tcttggagaa	aggctatgtc	cctctcaaag	atatgagcca	gttaacaaat	540
agctatctgg	aaacaaccct	cgactgggtt	ccaggaatga	aggatatccg	attaagggac	600

ttcccatcat	tcatcaggac	aacggatcca	aaagacatca	tgtacaat	cggtattaca	660
gaaaccgacg	ctgtctccag	agccaaagct	ctgatcatca	acacctttca	tacattggaa	720
cacgacgttg	taaatgccct	ctccaccatg	tttccacgtg	tttacaccat	cggctctctt	780
cagctgatgt	tggaccaagt	tcatgacaag	agccttaacg	ccatcaactc	caatctctgg	840
aaagaagaat	cgcaatgcat	cgattggctc	aattcaaaaag	agcccgaatc	cgtttgtgtat	900
gtgaatttcg	gtagtgtcac	tgttgtgact	gctcaacaac	tgacggaatt	tgcgtagggg	960
cttgccaaca	gcaacaagac	ttttttatgg	gttatttaggc	ctgatatagt	tgttggagac	1020
tcggcaatgc	tgccccctga	attcttgacg	gacacggaag	acagaagcat	gctaataagc	1080
tggtgtaacc	aagaacaggt	gttgaggcac	ccttccatcc	gaggattttt	gacgcacagt	1140
ggttggaaact	cgacgcttga	aagtattgtc	agcggagtgc	ctatgatatg	ttggcctttc	1200
tttgctgagc	aacagacaaa	ttgtaggttc	agttgcgtgg	aatgggaaat	aggaatggag	1260
attgacaata	atgtgaagag	agatgagggt	gaggtgctgg	tgagagagtt	gatggatggt	1320
gaaaagggga	agaaaatgaa	gaagaaagct	atggagtgga	agatgaaagc	agaagcagca	1380
gctgcccctg	ggggaccttc	gtctttaaat	ttggaaaaac	ttattgagga	ggtgcttttg	1440
caataa						1446

<210>22

<211>1308

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB660

<400>22

atgaaggctc	atgcagtgat	gcttccttgc	cccgatcaag	ggcacttaaa	tcctatgctg	60
aaactggcca	aaatatattgca	ttcaagaggc	ttcttcatca	cattcgtgaa	cacggaattc	120
aatcacaatc	gtctagtgcg	tgcgagaggc	cccgaatctg	ttaaaggctg	cgatgatttt	180
cagttcaaaa	ccataacctga	tggactaccg	ccttttgata	aggacgcaac	gcaagacata	240
cctcaactgt	gtgatttctt	tcaaaagaat	ggcttccttc	cattgttgga	cctcattaaa	300
agtattaatg	attcacccgga	ctgtccaaat	gttacctgta	tagtgattga	tttggccatg	360
agtttcgctc	ttgatgcggc	cgagggtgtc	aaaattccca	cgggtgtactt	ttcgccaact	420
agtgtctgtg	gattcatggg	gttttgcaat	tatgaagagc	ttgtgaatcg	aggattgttt	480
ccacttaaa	atgaaagtca	aataactaat	ggctatcttg	ataccaaact	agactgggtg	540
ccagggatga	agaacattag	gctcagagat	tttccatagt	tcatccgaac	gactgatcca	600
gatgatata	tggtgaactt	catgattttt	aacatgaaga	atgcgcctcg	tgcaaaggct	660

gtggtagtca acacattcga tgaattggag aaagatgtat tggaggccct aagtaaaaaa	720
tttgatcatg ttttttccat aggcccactc caattgatgg agaaggcttt ccaaagcct	780
gaggtaaaat ctataggatc aagcttgttg aaagaagaca acacgtgcat cgcctggctc	840
aacggcaggg agccaaattc tgtgtttgtac gtgaactttg gaagcatcac agtgtttgtca	900
cctcaacaac tattggagtt cgcatggggc ctagccaata gcaaccatta ctttttgttg	960
atcataaggc cagatttggg aagtggagaa tctgcgattt tatccgaaga gtactcaaag	1020
gaagtgaag ggcgggcat gatggtgcgt tgggtgctctc aagagcaagt attggcccat	1080
ccttcggtag gtggattctt gacacattct ggctggaact cgactatcga aggaatgtca	1140
gaaggtgttc ctatgatattg ttggcctttt ttgtctgacc aacagaccaa ttgtcggtat	1200
gcatgcacgg agtgggagat tggaatggag attgaaggag aggttacgag ggataaagtg	1260
gcggatttgg tgaatatatt gatggaggag ggaaggggag agcgatga	1308

<210>23

<211>1506

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB658

<400>23

atggccattc atgaacaaaa acctcacttt gtccctgttcc ctttcatggc acaaggccat	60
atgattccca tggtagatat cgccagatta ctgcggaagc gcggtgtcac aatcaccatt	120
ctactcacac cccacaatgc caacagggtc aaaacagtca ttgctcgtgc aatcgattca	180
ggactaaata tcaatgtcat ccacttcaaa tttccatccg ttgaggtcgg attgcccga	240
ggttgtgaga atttcgatat gctccctgac atcaatggcg cattgcagtt tttaaagcc	300
actttcatgt tacaagaaca ggtcgaagag ttgcttccaa agctcgagcc tcttccgagc	360
tgcctaattg ctgatattgt ctttccatgg acaacaaatc ttgctttgaa gttaaatgtt	420
ccaagaattg tgtttcacgg gacaagttgc ttttctctcc tatgtatgca cgtttttagga	480
acttctaagg atttcgaagg tgtgactaac gaaacggagt acttccttgt gcctggatta	540
ccagataaaa tcgaaataac caaaattcag cttaggggca cccttattca aatgaattca	600
gactggacga agtttcgtga tgagggtcga gaggctgagg taaaagcatt tggaacgggtg	660
gccaatattt ttgaagattt ggaaccagag tatgtcaaag aatacagcag agttaaaggc	720
aaaaaagtct ggtgcatagg tcctgtttca ttatgcaaca aagatggcat agacaaggcc	780
gaaagaggta acatggcttc aatcgacgca caccattgct tgaagtggct caattcacac	840
gaacaaaagt ctgttattta cgtctgcctt ggaagcatat ctgcctcgc tacttcacaa	900

ctgatagagc ttggattggc tttagaagca tcaaacagac cttttatttg ggtagttaga	960
gatccatcac aagaacttaa aaaatggttt ttgaatgaga aatttgagga aagggtaaag	1020
gatagaggcc ttttgatcaa cggttgggcg cctcaagtgc tcatacttc ccatccatct	1080
gttggagggt ttgtaacgca ctgctggctgg aactcgatgc ttgaagggt tacttcaggc	1140
ttgccgatga taacgtggcc tgtatttgct gagcagtttt gtaatgaaaa gtttattgtt	1200
cacgtgatca agactgggat aagagtgggt gttgaagtgc ctatcatctt tggagatgaa	1260
gaaaaagtcg gagttttggt gaagaatgat gagataaaga tggttataga taagttgatg	1320
gatggaggag aagagggaga agagagaaga gagagagctc aaaagcttgg agaaatggca	1380
aaaaaggcaa tggaggaggg tggttcttct tatcataatt tgacatcggt catgcaagat	1440
gtcatgatgc aacaagctaa taatggagat caatatgaag atggtgttac agttataaat	1500
acatga	1506

<210>24

<211>30

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1617BamHINcoI-FW

<400>24

gggggatcca tggctagtga gagccaaata	30
----------------------------------	----

<210>25

<211>36

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1617XhoIKpnI-RV

<400>25

cccctcgagg gtacctcaca aaacattatt cacgac	36
---	----

<210>26

<211>24

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1617-F

<400>26

atgggagaag aatacaagaa aaca

24

<210>27

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1617-R

<400>27

taaaatttgg tagttaaacc gatgta

26

<210>28

<211>1386

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1721

<400>28

atgctgagcc tcgccaaaat tctgcaccaa aagggtattcc atatcacttt cgttaacact 60

gaatttaacc atgaacgcct cctgagaacg agaggcccga attcccttga cgggttgccct 120

tcgtttcgat tcgagacaat tcccgacggt cttccgccat cagaccccga tgctacacaa 180

aacgttgcatt tattgtttga gtccagcaca tccaaatgct tagctccatt cagggacctt 240

cttgctaagc taaaccacac cgacgtgccg ccagttactt gcatactatc cgacttaatc 300

atgagcttca ctcttgaagc tgctcaagag ctcagcatcc ctgatgtcct tttttggacc 360

gctagcgtt gtggatacct cgcttatgca cactatgccg cgcttattga aaaaggattt 420

acacctttca aagatacgag ttgcttgacc aatgggtatt tggataccgt tattgatgat	480
attcctagtc tggaaggcat acgtctgaga gacattccaa gttttatcag aacaactaat	540
ccagatgaca ttttgatgaa ctttgtgttg cgagaaacag agagagctag aaaagggtcc	600
gccgtaatct ttaacacgtt cgagtgcctc gaggttgaag cattaacgt actttcatcc	660
atgttgcctc cagtttacac agttggaccc ctgcatttgg ttgaaaagca tgttggtcac	720
aaaggattgg aggtgcttgg atcaaattta tggaaagaag agccaaaatg tctcgaatgg	780
cttgactccc aaattcccaa ctgagtgggt tacgttaatt ttggaagcat cgctgtcatg	840
acaactgacc aactgattga gttttcttgg ggtcttgcta atagcaacat atccttcttg	900
tggattataa gacctgacct tgtctcaggg gaaaacgctg ttcttccacc cgaatttctc	960
gaagccacaa aagaaagagg gtgttttagca aattgggtgcc ctcaagagaa agttcttagc	1020
cacccatcca tcagaggatt cttaactcac agcggatgga attcaactct tgagagcatt	1080
tgcagtggag ttccaatgat cagttggccg ttcttcgccg aacaacagac taactgttgg	1140
ttttgctgca caaatgggg cataggcata gagctagaca atgatgtcaa aagggataaa	1200
gtggaagacc ttgtgcgcga attgatgtct ggggataaag ggaaagagat tatgaaaatg	1260
gctatggagt ggaagaagct ggccgaagag tctgccaga gttcatcttt taagaatcta	1320
gagaaagtga ttcatgaagt gcttttacca ccactacaag tgtgggatcc taaggattcc	1380
acctaa	1386

<210>29

<211>1374

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1724

<400>29

atggaggaca ctatcgttct ctacgcttca gcagagcacc ttaactccat gctactactc	60
ggcaaactca tcaacaaaca ccaccccaca atctccgtcg ccattatcag caccgcccc	120
aacgccgccg ctagttccgt cgccgacgtg gcggccatat cttatcagca actcaaaccg	180
gccactctcc cttcggatct aaccaaaaac ccaatcgagc tcttcttcga aatcccacgt	240
ctacataatc ctaacttgct cgaagcgctg gaagaactgt cactaaaatc aaaagtaagg	300
gcatttgtga tagatttctt ttgcaatccc gcatttgagg ttctgactag cttgaacata	360
cccacttact tctatgtcag cagcggcgcg tttgggctat gcgggttctt gcattttccg	420
acaatcgacg aaactgtcga aaaagacatc ggtgaactga acgatatctt ggagatcccg	480
ggttgccccc cggttttgtc ctcggatttt ccgaaaggta tgttctttcg caagagtaac	540

acttacaagc atttttttaga cacggcgaaa aacatgagga gagcgaaagg gatcgtgggtg	600
aacgccttcg acgcgatgga gttccgagct aaagaagccc tcgtcaacaa tctgtgcgta	660
cccaattcgc caactccccc agttttctta gtcggcccat tggtcggagc aagcacaact	720
acgaaaacca caaacgaaca gcacgaatgc ttgaaatggc tggacgtgca gccagacaga	780
agcgtgatct tcttatgttt cggtaggagg ggtttgttct ccgcagacca attgaaggaa	840
atcgcaattg gtctggagaa cagcggccac aggttcctgt ggtccgtgcg ttgcccacca	900
agtaagccta actcttataa cactgatccg gacctggacg agctcctgcc cgaggggttt	960
ttgtccagga ccgagacccg gggtttcgtg atcaagtcgt gggcgcctca gaaggagggtg	1020
ctgagccatg gcgcggttgg agggttcgtg acgcactgtg ggaggagtgc gatattggaa	1080
gcggtgtcgt ttgggggtgcc gatgatcggg tggccgatat acgcggagca gaggatgaat	1140
agggtgttca tgggtggagga gatgaagggt gcgttgcagt tggatgaggt ggaggaaggg	1200
ttcgtggcgg cgggtggaatt ggagaagaga gtgaaggagt tgatggattc gaagaatggg	1260
agagcggtta ggcagagagt gaaggagatg aaagtggcgg ctgaggtggc ggttgaaaag	1320
ggtggttcgt cagttgtggc gttgcaacgc tttgttgata tgggtggtttc ttaa	1374

<210>30

<211>1362

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1723

<400>30

atggaggcag acaaagaaaa tctcaagatt ttaatgttcc catggttggc tcatggtcatt	60
atatttccat ttcttgagct agccaaaaga atcttgaagc gaaaaaactg gcacatatac	120
ttgtgtacca cagccataaa cttcagttct atcaacaact tcattgaaaa atataagttg	180
gagaactcaa tagaagtagt agaactccat atagaacat cccctgaact tccacctcat	240
taccacacta caaagaattt gccacaagt ctcaattcta ccctattaaa ggccattcag	300
acgtcgaatt cgagcttctc agacatcatc agaacattga aacctgaact agtcatatat	360
gatgtgtttc aaccttgggc tgccaagatt gcttcctcac aaggatttcc tgctgtttat	420
ttttctagct ttggaggggc accattatca cttatgcac atcaccacac gtacggaaaa	480
cccgaatttc cttccaagc aatagttgtt gaggacatcg aactggaaag tttgctctct	540
ttgtttgatt tcttgtatgc caacatattt gaagtggatc aagattatct ttttggaat	600
ttcaagcaat cttgtgagct tgttttgtta aagagtagta aagggttga gaggaagtac	660
atcgattatc tttcatcttt gtctcagaaa aaaatattac ctgttggacc actagtcaca	720

gttgacaata agaccaatga ggagaattcc gagatcatga attggttgag caagaaaaaa	780
caccattcaa ctgtctacat ttccttcggt agtgaatact tcctgtctaa agaagagatt	840
gaagagatag caaaagggct tgagctttgt gatgttaact ttatatggat catcagattt	900
ccagttggag tgaccgttaa cttagaagaa acactgcctc aaggtttcct tcaaaggggtg	960
aacgaacggg ggatggttgt ttcaggatgg gcaccacaga gcaacatatt agcacatcca	1020
agcacaggag gctttgtgag tctactgtggg tggagtctta tcacagaaag cgtatatattt	1080
ggtgttcggg tcatagggat ggcaatgaaa cttagatcagc caataaacgc cagaatgtta	1140
tcagaggctg gtagtttgtt cgaagtcaaa agatatgaaa atgaagtgtt taggggagaa	1200
gagatagcga aggcgataaa gaaggtgatt gttgaggaca gtggagaaag gctgcggcaa	1260
agagcttttag aattgagcga gaagatgaaa atggaagagg aaaatgagat ggatgaagta	1320
actgagcagc tgtgggagct ttgcttgacg aaaaaacggt aa	1362

<210>31

<211>1437

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB1719

<400>31

atggaacctc atatagttat attcccgttc atgtccaaag gccacacaat cccctctcctc	60
cacctctccc acctcctcct tagtcgcgga gtacgcgtaa cgatcttcac cactgcacaa	120
aaccaccctt tcatcgctca acatgtccca aaaacaaata atgttaccat cattgacct	180
ccgttccttg ataacatccc tggaatttca ccaggaacgg agagcacgga caaactccc	240
tcgatgtctc tcttcgtccc gttcgtgaac gccgctaaat cgatgcaacc gttcttcgaa	300
gatgagcttg agaaaattca ttcaggggtt agttgtgtta tatcggatgg ttttcttcat	360
tggacgctga aatcagcatc caagttcgga attccacgac tgagtttcta cggtatgagc	420
tactatgcct tgacaatttt tcgagtcgct atctcaaaca agttaatatc attgcacgag	480
tcaccgcacg aggcatcac cttacctagt tttccttgga ttaaactcac tagagatcac	540
ttcgacaaac cacttgatca acgtgaacca aatgggccgc aatttgactt tttcatggaa	600
gcaacgacag ctactgtgaa tagctatggt ttcttagtga atagcttcta tgagcttgaa	660
ccaactttcg cggattacta tgacaacaat tacaaccca aggcgtggag tgcgggcct	720
ctctgcctcg cacaaacgcc aaagaatgat aatctctcgt cgaagcctga gtggattcat	780
tggcttgacc aaaagttgga acaagatcgc cctgttttgt acattgcatt cggatcacia	840
gcagaaatta cactagaaca gttacatgaa atctcacgag ggttggaaga gtcaaatgta	900

cactttttgt	gggttttaag	gaacaatgga	gttgaactaa	gtgatggatt	tgaagacagg	960
gttaagaata	gaggaattgt	agtaaaagaa	tgggttgatc	aaagagagat	tcttgaacat	1020
gaaagtgtaa	aaggctttct	aagtcattgc	ggctggaatt	cggtaatgga	aggtatatgt	1080
gcgagggttc	tgattcttgc	gtggccaatg	atagcggagc	aacacttgaa	tgcaaagatg	1140
gtgagtgaag	aaataaagat	tggtttgaga	gttgaaacgg	ttgatggaac	ggcaaaggga	1200
tttgtgactg	cggcgagttt	gacgaaggcg	gtgatggaat	tgatggaggg	tgagaagggg	1260
aaggaattga	gggagaatgt	gaagaaagtg	gcgggggcag	cgagggaagc	ggtggtggaa	1320
ggtggttcgt	cgtggaatgg	tttgaatgaa	ctcattgatg	aggtgtgtag	gcataaggaa	1380
atgagtggta	gttctaaagt	tgatgaaaac	aagagggaaa	ttaaggatat	taattaa	1437

<210>32

<211>24

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1725-NcoI

<400>32

cccatgggag aagaatacaa gaaa

24

<210>33

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 1725-KpnI

<400>33

ggtacctata aaatttggtg gttaaa

26

<210>34

<211>1080

<212>DNA

<213>

<220>

<221>

<222>

<223>GAPDH

<400>34

caccgattac atgacgtaca tgttcaagta cgacagtgtt catggtcagt ggaaacacca	60
cgagttgaag gtacaggatg agaagaccct tctgtttggt gaaaagccag taagagtctt	120
gtcaactggt gtcttcacgg acaaagataa ggctgctgct cacttgaagg gtggtgccaa	180
gaaggttgtg atctcagcac caagcaaaga tgcaccaatg tttgttgtgg gtgtcaatga	240
gaaggaatac aaaccagagt tggacattgt ttccaatgct agttgcacta ccaattgcct	300
tgccccctttg gccaaaggta ttaatgatag atttggaatt gttgagggcc tcatgaccac	360
cgtccactct attaccgcaa ctcaaaagac tgtcgatggg ccatcgagca aggactggag	420
aggtggaaga gctgcatcgt tcaacattat ccccagcagc actggtgcag ctaaggctgt	480
tggtaaagtg ctcccagttc tcaatggaaa gctaacggga atggccttcc gtgttcctac	540
tgtcgatgtc tccgtagtgg acctcactgt caggctcgag aaagaggcca cttatgatga	600
gatcaaagct gctatcaagg aggaatccga gggcaacctt aagggcattt tgggctatac	660
cgaagatgat gtggtgtcaa cagactttgt tggatgatag cgatcaagca ttttcgatgc	720
caaggctgga attgcattga gcaagacgtt tgtgaagcct gtgtcgtggt acgacaacga	780
atgggggttac agttcccgtg tgatcgacct gatcgtgcac atggcctcag tttctaaggc	840
ttgatcgatg atctgcttag gccgtgaagc agcttttgtc ttatcgcatc ttttctgagt	900
ttgtaataat gggcttttgt gttatttgca gcctaatttt gcagtttgca aatttatggt	960
ttttggttat gttttgctga aacctatttt attacccttt cgcgttgggt tattgaatgt	1020
gaactctttt tactgatgtg tttaacgttc tctcttttaa aaaaaaaaaa aaaaaaaaaa	1080

<210>35

<211>20

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer AmGAPDH-F

<400>35

tgttgctggt aacgatccat

20

<210>36

<211>18
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer AmGAPDH-R
 <400>36
 agctcttcca cctctcca

18

<210>37
 <211>24
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer AmAS-F
 <400>37
 atgttcaaaa atcctaatat ccgc

24

<210>38
 <211>25
 <212>DNA
 <213>Artificial Sequence
 <220>
 <221>
 <222>
 <223>Primer AmAS-R
 <400>38
 ttagccatca agctcaatct tgaca

25

<210>39
 <211>16
 <212>DNA
 <213>Artificial Sequence

<220>

<221>

<222>

<223>M13 reverse primer

<400>39

aacagctatg accatg

16

<210>40

<211>24

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer ThDFR-NcoI

<400>40

gctttacat ggagtaatga gctt

24

<210>41

<211>1367

<212>DNA

<213>

<220>

<221>

<222>

<223>pSPB266(ThF3H)

<400>41

gtatgtatgt atgtatgcta tatacgagtc gataaagttg atcgttttca ttttcgacaa 60
atacaaacct cgtgagagaa tcttctcgat catatggcac gagcaggacc actaaccta 120
acttcgctag cgctcgagaa atcgctgcat gaaaagttaa taaggacga agacgagagg 180
cctaacttag catacgatca atttagcagt cagattccat tgatctctct ctctgggatc 240
gacgatgaat gtaataagag gaaagagctg tgcaagagaa tagcgcaggc atgcgaagat 300
tggggatattt ttcaagtgat cgatcatggg atcgatttga aactcgtcaa cgatatgact 360
cgtttggtc gtgagttctt cgatttgccc gacgaagaga agctgagggt cgatatgtct 420
gggtgggagaa aaggagggtt cattgtttcg agccaccttc agggcgagggt ggtccaagac 480
tggcgcgaga tcgtgacctt cttcacatac cctatcaaag gccgtgacta ttccctgtgg 540

cccgacaagc ccgaggcatg gcgggccgtg acagagacct acagctcgca gctaattgtgc	600
ctgggctgca aattgctagg aatcctatcc gaggcaatgg gcctcgaaag agaâgçgctg	660
accaaggcct gtctgaacat ggaccaaaaa gttgtggtca acttttaccç aaaatgcçct	720
cagcccaatt tgacattggg cctgaagagg cactcggacc caggtttgat cactctgctg	780
tttcaggata acgttggcgg gcttcaagcg actcgagacg gcgggaagtc gtggatcacg	840
gtccagcccc ttgagggtgc attcgtggtc aatcttggtg attttgctca ttacttgagc	900
aatggaaggt tcaagaacgc ggatcatcga gcggtggtga attcaaacac gaatagaatg	960
tcgatcgçga çgtttcaaaa cccatcgcca gaggctatcg tgtaccctct caagatcgga	1020
gacgacggga agccçattat agaaaagccc atcacttatg gagaaatgta caagaggaag	1080
atggçtaaaç acattgaact tgccaagctc aagaagçtag ccaaggaaca aaagttgcaa	1140
gaagaagttg ttaataatgt tgaagatcat catçttaaca atgggaaaac taaataggag	1200
gttaaggtct ttaaggaaac tgacgttgtc ttgtgattgt tatatattct çtatgtçgta	1260
) ttçgtçttaa ggttgtcaga tgaaaatatc gaccatgtta ggtatttaat ttatatgaat	1320
tgtattgçct agtcggccat attatgatta aaaaaaaaaa aaaaaaa	1367

<210>42

<211>22

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer ThF3H-Sall-1

<400>42

) ttçtçtgtcg acgçççattg çç

22

<210>43

<211>22

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer ThF3H-Sall-2

<400>43

çgççgtgtçg actçgçttga ag

22

<210>44
<211>24
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer AmAS-INSITU-FW
<400>44
aattattttcc caatgttcaa aaat

24

) <210>45
<211>21
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer AmAS-INSITU-RV
<400>45
tggagcttta ggtttgtgaa a

21

) <210>46
<211>23
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer KIR-INSITU-FW
<400>46
atgggagaag aatacaagaa aac

23

<210>47
<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer KIR-INSITU-RV

<400>47

tcttacgata aaacaaactc a

21

<210>48

<211>19

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer T.F3H-923F

<400>48

atcatcgagc ggtggtgaa

19

<210>49

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer T.F3H-1339R

<400>49

tggccgacta ggcaatacaa t

21

<210>50

<211>22

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer T.GAPDH-F87

<400>50

cccttctgtt tggtgaaaag cc

22

<210>51

<211>22

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer T.GAPDH-R692

<400>51

cctcggattc ctccttgata gc

22

<210>52

<211>29

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 417-NcoI

<400>52

cccatatata gccatggaag ataccatcg

29

<210>53

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer 409 EcoRI

<400>53

tagtggtgtg gagtcggggg atttcg

26

<210>54

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer SWB DFR-1158F

<400>54

aatgggatgc ttccgacttc t

21

<210>55

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer SWB DFR-1223R

<400>55

cagtggtttc tgccattgct t

21

<210>56

<211>20

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Probe SWB DFR-1180T

<400>56

aggaaaaaac aggctgaaaa

20

<210>57
<211>19
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer Torenia F3H-1035F
<400>57
catcgagcgg tggatgaatt

19

<210>58
<211>19
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Primer Torenia F3H-1101R
<400>58
ctggcgatgg gttttgaaa

19

<210>59
<211>19
<212>DNA
<213>Artificial Sequence
<220>
<221>
<222>
<223>Probe Torenia F3H-1055T
<400>59
aaacacgaat agaattgtcg

19

<210>60
<211>22
<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer AmAS-1545F

<400>60

gaagatgacc ttgcggtgat tt

22

<210>61

<211>25

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer AmAS-1638R

<400>61

ttgtcctcctt cccctttata ggttt

25

<210>62

<211>26

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Probe AmAS-1582T

<400>62

agttcgccgg gagtttcgtg agtctg

26

<210>63

<211>17

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer AmGTcg12-908F

<400>63

ggttggcccg catttca

17

<210>64

<211>20

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer AmGTcg12-966R

<400>64

tagaaaaccc tccggcagaa

20

<210>65

<211>17

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Probe AmGTcg12-929T

<400>65

agatggactt aaatgcg

17

<210>66

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer SWB GAPDH-794F

<400>66

gcattgagca agacgtttgt g

21

<210>67

<211>21

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Primer SWB GAPDH-859R

<400>67

acgggaactg taacccatt c

21

<210>68

<211>18

<212>DNA

<213>Artificial Sequence

<220>

<221>

<222>

<223>Probe SWB GAPDH-816T

<400>68

agcttgtgtc gtggtacg

18

<210>69

<211>2220

<212>DNA

<213>Linaria bipartita

<220>

<221>CDS

<222>(127)...(1488)

<223>Nucleotide sequence of cDNA encoding 4'CGT of linaria bipartita

<400>69

tggacactga catggactga aggagtagaa ataccaaaag ttttcaaact ctttattgca

60

atatacttgt acaaatctac tgcaactaaa acctattatt aattatatat ataccatat

120

ata gat atg gaa gat acc atc gta ttt tac act cca agc gat cac agt

168

Met	Glu	Asp	Thr	Ile	Val	Phe	Tyr	Thr	Pro	Ser	Asp	His	Ser			
1				5					10							
caa	ccc	aca	ata	gcg	ttg	gca	aag	ttc	atc	agc	aaa	cac	cac	cct	tcc	216
Gln	Pro	Thr	Ile	Ala	Leu	Ala	Lys	Phe	Ile	Ser	Lys	His	His	Pro	Ser	
15				20				25						30		
atc	tcc	atg	aca	atc	atc	agc	acc	gcc	gca	ttc	cct	tcg	tcc	gca	gcg	264
Ile	Ser	Met	Thr	Ile	Ile	Ser	Thr	Ala	Ala	Phe	Pro	Ser	Ser	Ala	Ala	
				35				40						45		
gtg	ctg	cct	aaa	aca	ata	agt	tac	cac	ccc	ctc	ccc	gcc	gtg	ccc	atg	312
Val	Leu	Pro	Lys	Thr	Ile	Ser	Tyr	His	Pro	Leu	Pro	Ala	Val	Pro	Met	
				50				55					60			
ccc	ccg	aac	ctc	tcc	tcc	aat	ccc	gtg	gaa	ttc	ctc	ttc	gaa	atc	ccc	360
Pro	Pro	Asn	Leu	Ser	Ser	Asn	Pro	Val	Glu	Phe	Leu	Phe	Glu	Ile	Pro	
				65				70					75			
cga	ctc	cac	aac	act	aaa	ctc	cgc	gaa	gca	ctc	gaa	aga	atc	tcc	gag	408
Arg	Leu	His	Asn	Thr	Lys	Leu	Arg	Glu	Ala	Leu	Glu	Arg	Ile	Ser	Glu	
				80				85					90			
aca	tca	aag	atc	aag	gcg	ttg	ggt	atc	gat	ttc	ttt	tgc	aac	tcc	gct	456
Thr	Ser	Lys	Ile	Lys	Ala	Leu	Val	Ile	Asp	Phe	Phe	Cys	Asn	Ser	Ala	
				95				100					105		110	
ttc	gaa	gtt	tcc	agg	agc	ttg	aac	att	ccg	aca	ttc	ttc	gaa	gcc	agc	504
Phe	Glu	Val	Ser	Arg	Ser	Leu	Asn	Ile	Pro	Thr	Phe	Phe	Glu	Ala	Ser	
				115				120					125			
ctc	ggc	gcg	tcc	ggg	ctc	tgc	gag	ttt	ctc	tac	cac	ccg	aca	ttt	cac	552
Leu	Gly	Ala	Ser	Gly	Leu	Cys	Glu	Phe	Leu	Tyr	His	Pro	Thr	Phe	His	
				130				135					140			
aaa	acc	gtc	ccc	gga	gac	atc	gcg	gac	ttc	aac	gac	ttt	ctt	gaa	atc	600
Lys	Thr	Val	Pro	Gly	Asp	Ile	Ala	Asp	Phe	Asn	Asp	Phe	Leu	Glu	Ile	
				145				150					155			
ccg	ggg	tgc	cct	ccg	ctt	cac	tcg	gct	gat	gtc	cct	aag	ggt	ttg	ttc	648
Pro	Gly	Cys	Pro	Pro	Leu	His	Ser	Ala	Asp	Val	Pro	Lys	Gly	Leu	Phe	
				160				165					170			
cga	cgc	aag	act	att	gct	tac	aaa	cac	ttc	ctc	gac	act	gcc	aac	aac	696
Arg	Arg	Lys	Thr	Ile	Ala	Tyr	Lys	His	Phe	Leu	Asp	Thr	Ala	Asn	Asn	
				175				180					185		190	
atg	cgg	atg	tcg	agt	gga	atc	ctc	tta	cac	gcg	ttc	gat	gcg	ctt	gaa	744

Met Arg Met Ser Ser Gly Ile Leu Leu His Ala Phe Asp Ala Leu Glu	
195 200 205	
tac cga gct aag gaa gct ttg tcc aac ggc ttg tgc aat ccg gac ggg	792
Tyr Arg Ala Lys Glu Ala Leu Ser Asn Gly Leu Cys Asn Pro Asp Gly	
210 215 220	
cca act ccg cct gtt tac ttt gtt tcg cct act gtg gct gaa aca ttg	840
Pro Thr Pro Pro Val Tyr Phe Val Ser Pro Thr Val Ala Glu Thr Leu	
225 230 235	
gca tac agg gaa aac acc gcc gcc ttg cgg cat gaa tgc ttg acg tgg	888
Ala Tyr Arg Glu Asn Thr Ala Ala Leu Arg His Glu Cys Leu Thr Trp	
240 245 250	
ctt gat ttg cag cct gat aaa agc gtt atc ttc ctt tgt ttt gga agg	936
Leu Asp Leu Gln Pro Asp Lys Ser Val Ile Phe Leu Cys Phe Gly Arg	
255 260 265 270	
agg gga aca ttc tcc atg caa cag ttg cat gaa att gct gtc ggt ctt	984
Arg Gly Thr Phe Ser Met Gln Gln Leu His Glu Ile Ala Val Gly Leu	
275 280 285	
gaa cgg agc ggg cga aga ttt ctc tgg gcc atc cgc agt agt ggg gca	1032
Glu Arg Ser Gly Arg Arg Phe Leu Trp Ala Ile Arg Ser Ser Gly Ala	
290 295 300	
ggg aac ggt gag cct gac ttg agc gtg gtg ctg ccg gag ggt ttc ttg	1080
Gly Asn Gly Glu Pro Asp Leu Ser Val Val Leu Pro Glu Gly Phe Leu	
305 310 315	
gag aga acc aaa gat att ggg ctg gtg ata acg aca tgg gcg ccg cag	1128
Glu Arg Thr Lys Asp Ile Gly Leu Val Ile Thr Thr Trp Ala Pro Gln	
320 325 330	
aaa gag gtg tta agc cat gtg gcc gtg tgt gga ttt gtg acg cac tgc	1176
Lys Glu Val Leu Ser His Val Ala Val Cys Gly Phe Val Thr His Cys	
335 340 345 350	
ggc tgg aac tca gtt ctc gag gcg gtg tcg ttt ggg gtt ccg atg att	1224
Gly Trp Asn Ser Val Leu Glu Ala Val Ser Phe Gly Val Pro Met Ile	
355 360 365	
ggg tgg ccg ctg tac gca gag cag agg atg aat cgg gtg ttt atg gtg	1272
Gly Trp Pro Leu Tyr Ala Glu Gln Arg Met Asn Arg Val Phe Met Val	
370 375 380	
gag gaa ata aag gtg gca ttg cct ttg gag gag gag gcg gat ggg ttg	1320

Glu Glu Ile Lys Val Ala Leu Pro Leu Glu Glu Glu Ala Asp Gly Leu	
385	390
395	
gtg agg gcg aca gaa ttg gag aag cgg gtg aga gag ttg acc gag tcc	1368
Val Arg Ala Thr Glu Leu Glu Lys Arg Val Arg Glu Leu Thr Glu Ser	
400	405
410	
gtg agg gga aaa gcg gta agc cgg cgg gtg gag gaa atg aga ctc tcg	1416
Val Arg Gly Lys Ala Val Ser Arg Arg Val Glu Glu Met Arg Leu Ser	
415	420
425	430
gca gag aag gcc gtg agc aag ggt gga acg tcg ctg att gca ttg gag	1464
Ala Glu Lys Ala Val Ser Lys Gly Gly Thr Ser Leu Ile Ala Leu Glu	
435	440
445	
aaa ttc atg gac tcg att act cta taagcgtaag agttgctata aatttagcta	1518
Lys Phe Met Asp Ser Ile Thr Leu	
450	
tgttgcacgg atacgtcaaa taaaccttgc tcgtattctt agatacgtat actatacaaa	1578
tacaatttat gaataagttt ttcataatggc gtatgaagta ttctaattaa attaaataac	1638
acgtttttgaa gcgttattat aagggcgtaa ctagtaaata ataagaaata attaaacaaa	1698
aaaaaattat gatgttaatg ataattttat taatatttta tactataaag ttcttaatat	1758
tcttgttgat atgtaagttt attatataag tattttaagt gttttatttg gtattttgaa	1818
tttaagtacc atcgtggaat actttttatat gagcttataa ttttaatggtt gaatagattt	1878
catattaata tgttattatt tatgtgaaca aaaaatatta ttgctcaagt tattttgaat	1938
tatattttta tatatataag tatttgatat aaaatattta acgtattatg tgcgtatcct	1998
tatttttaca agttaccctg attcgtttca tgtttgatac attttttcat attcgtatat	2058
gtgcccgtgt ccgtgcaata tagtaaatta gttatggat gtgatgtttc tatgttgtaa	2118
caaaataatg gtacttaatt tgaatagtc agtcaagtat ttgtaatggt aaattaatat	2178
tccatttaat attccattat tctctcaaaa aaaaaaaaaa aa	2220

<210>70

<211>454

<212>PRT

<213>Linaria bipartita

<220>

<223>Amino acid sequence of 4'CGT of linaria bipartita

<400>70

Met Glu Asp Thr Ile Val Phe Tyr Thr Pro Ser Asp His Ser Gln Pro
1 5 10 15

Thr Ile Ala Leu Ala Lys Phe Ile Ser Lys His His Pro Ser Ile Ser
 20 25 30
 Met Thr Ile Ile Ser Thr Ala Ala Phe Pro Ser Ser Ala Ala Val Leu
 35 40 45
 Pro Lys Thr Ile Ser Tyr His Pro Leu Pro Ala Val Pro Met Pro Pro
 50 55 60
 Asn Leu Ser Ser Asn Pro Val Glu Phe Leu Phe Glu Ile Pro Arg Leu
 65 70 75 80
 His Asn Thr Lys Leu Arg Glu Ala Leu Glu Arg Ile Ser Glu Thr Ser
 85 90 95
 Lys Ile Lys Ala Leu Val Ile Asp Phe Phe Cys Asn Ser Ala Phe Glu
 100 105 110
 Val Ser Arg Ser Leu Asn Ile Pro Thr Phe Phe Glu Ala Ser Leu Gly
 115 120 125
 Ala Ser Gly Leu Cys Glu Phe Leu Tyr His Pro Thr Phe His Lys Thr
 130 135 140
 Val Pro Gly Asp Ile Ala Asp Phe Asn Asp Phe Leu Glu Ile Pro Gly
 145 150 155 160
 Cys Pro Pro Leu His Ser Ala Asp Val Pro Lys Gly Leu Phe Arg Arg
 165 170 175
 Lys Thr Ile Ala Tyr Lys His Phe Leu Asp Thr Ala Asn Asn Met Arg
 180 185 190
 Met Ser Ser Gly Ile Leu Leu His Ala Phe Asp Ala Leu Glu Tyr Arg
 195 200 205
 Ala Lys Glu Ala Leu Ser Asn Gly Leu Cys Asn Pro Asp Gly Pro Thr
 210 215 220
 Pro Pro Val Tyr Phe Val Ser Pro Thr Val Ala Glu Thr Leu Ala Tyr
 225 230 235 240
 Arg Glu Asn Thr Ala Ala Leu Arg His Glu Cys Leu Thr Trp Leu Asp
 245 250 255
 Leu Gln Pro Asp Lys Ser Val Ile Phe Leu Cys Phe Gly Arg Arg Gly
 260 265 270
 Thr Phe Ser Met Gln Gln Leu His Glu Ile Ala Val Gly Leu Glu Arg
 275 280 285
 Ser Gly Arg Arg Phe Leu Trp Ala Ile Arg Ser Ser Gly Ala Gly Asn
 290 295 300

Gly Glu Pro Asp Leu Ser Val Val Leu Pro Glu Gly Phe Leu Glu Arg
 305 310 315 320
 Thr Lys Asp Ile Gly Leu Val Ile Thr Thr Trp Ala Pro Gln Lys Glu
 325 330 335
 Val Leu Ser His Val Ala Val Cys Gly Phe Val Thr His Cys Gly Trp
 340 345 350
 Asn Ser Val Leu Glu Ala Val Ser Phe Gly Val Pro Met Ile Gly Trp
 355 360 365
 Pro Leu Tyr Ala Glu Gln Arg Met Asn Arg Val Phe Met Val Glu Glu
 370 375 380
 Ile Lys Val Ala Leu Pro Leu Glu Glu Glu Ala Asp Gly Leu Val Arg
 385 390 395 400
 Ala Thr Glu Leu Glu Lys Arg Val Arg Glu Leu Thr Glu Ser Val Arg
 405 410 415
 Gly Lys Ala Val Ser Arg Arg Val Glu Glu Met Arg Leu Ser Ala Glu
 420 425 430
 Lys Ala Val Ser Lys Gly Gly Thr Ser Leu Ile Ala Leu Glu Lys Phe
 435 440 445
 Met Asp Ser Ile Thr Leu
 450